

Schmidt, M.  
1635

#5

PAGE: 1

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/377,795

DATE: 04/05/2000  
TIME: 12:53:39

Input Set: I377795.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

ENTERED

P.S.

1 <110> APPLICANT: Karin, Michael  
2 Rothwarf, David M.  
3 Zandi, Ebrahim  
4 <120> TITLE OF INVENTION: Gamma Subunit of Cytokine Responsive Ikb-Alpha Kinase  
5 Complex and Methods of Using Same  
6 <130> FILE REFERENCE: P-UD 3613  
7 <140> CURRENT APPLICATION NUMBER: US/09/377,795  
8 <141> CURRENT FILING DATE: 1999-08-20  
9 <150> EARLIER APPLICATION NUMBER: 60/097,418  
10 <151> EARLIER FILING DATE: 1998-08-20  
11 <160> NUMBER OF SEQ ID NOS: 19  
12 <170> SOFTWARE: PatentIn Ver. 2.0  
13 <210> SEQ ID NO 1  
14 <211> LENGTH: 1994  
15 <212> TYPE: DNA  
16 <213> ORGANISM: Homo sapiens  
17 <220> FEATURE:  
18 <221> NAME/KEY: CDS  
19 <222> LOCATION: (149)..(1408)  
20 <400> SEQUENCE: 1

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21 ggccacgagca tggcccttgt gatccaggtg gggaaactaa ggcccagaga agtgaggacc 60  
22 ccgcagacta tcaatcccag tctcttcccc tcactccctg tgaagctctc cagcatcatc 120  
23 gaggtcccat cagcccttgc cctgttgg atg aat agg cac ctc tgg aag agc 172  
24 Met Asn Arg His Leu Trp Lys Ser  
25 1 5  
26 caa ctg tgt gag atg gtg cag ccc agt ggt ggc ccg gca gca gat cag 220  
27 Gln Leu Cys Glu Met Val Gln Pro Ser Gly Gly Pro Ala Ala Asp Gln  
28 10 15 20  
29 gac gta ctg ggc gaa gag tct cct ctg ggg aag cca gcc atg ctg cac 268  
30 Asp Val Leu Gly Glu Ser Pro Leu Gly Lys Pro Ala Met Leu His  
31 25 30 35 40  
32 ctg cct tca gaa cag ggc gct cct gag acc ctc cag cgc tgc ctg gag 316  
33 Leu Pro Ser Glu Gln Gly Ala Pro Glu Thr Leu Gln Arg Cys Leu Glu  
34 45 50 55  
35 gag aat caa gag ctc cga gat gcc atc cgg cag agc aac cag att ctg 364  
36 Glu Asn Gln Glu Leu Arg Asp Ala Ile Arg Gln Ser Asn Gln Ile Leu  
37 60 65 70  
38 cgg gag cgc tgc gag gag ctt ctg cat ttc caa gcc agc cag agg gag 412  
39 Arg Glu Arg Cys Glu Glu Leu Leu His Phe Gln Ala Ser Gln Arg Glu  
40 75 80 85  
41 gag aag gag ttc ctc atg tgc aag ttc cag gag gcc aag aaa ctg gtg 460  
42 Glu Lys Glu Phe Leu Met Cys Lys Phe Gln Glu Ala Arg Lys Leu Val  
43 90 95 100  
44 gag aga ctc ggc ctg gag aag ctc gat ctg aag agg cag aag gag cag 508

PAGE: 2

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/377,795

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TIME: 12:53:39

Input Set: I377795.RAW

45	Glu Arg Leu Gly Leu Glu Lys Leu Asp Leu Lys Arg Gln Lys Glu Gln	
46	105 110 115 120	
47	gct ctg cgg gag gtg gag cac ctg aag aga tgc cag cag cag atg gct	556
48	Ala Leu Arg Glu Val Glu His Leu Lys Arg Cys Gln Gln Gln Met Ala	
49	125 130 135	
50	gag gac aag gcc tct gtg aaa gcc cag gtg acg tcc ttg ctc ggg gag	604
51	Glu Asp Lys Ala Ser Val Lys Ala Gln Val Thr Ser Leu Leu Gly Glu	
52	140 145 150	
53	ctg cag gag agc cag agt cgc ttg gag gct gcc act aag gaa tgc cag	652
54	Leu Gln Glu Ser Gln Ser Arg Leu Glu Ala Ala Thr Lys Glu Cys Gln	
55	155 160 165	
56	gct ctg gag ggt cgg gcc cgg gcg gcc agc gag cag gcg cgg cag ctg	700
57	Ala Leu Glu Gly Arg Ala Arg Ala Ala Ser Glu Gln Ala Arg Gln Leu	
58	170 175 180	
59	gag agt gag cgc gag gcg ctg cag cag cag cac agc gtg cag gtg gac	748
60	Glu Ser Glu Arg Glu Ala Leu Gln Gln Gln His Ser Val Gln Val Asp	
61	185 190 195 200	
62	cag ctg cgc atg cag ggc cag agc gtg gag gcc gcg ctc cgc atg gag	796
63	Gln Leu Arg Met Gln Gly Gln Ser Val Glu Ala Ala Leu Arg Met Glu	
64	205 210 215	
65	cgc cag gcc gcc tcg gag gag aag agg aag ctg gcc cag ttg cag gtg	844
66	Arg Gln Ala Ala Ser Glu Glu Lys Arg Lys Leu Ala Gln Leu Gln Val	
67	220 225 230	
68	gcc tat cac cag ctc ttc caa gaa tac gac aac cac atc aag agc agc	892
69	Ala Tyr His Gln Leu Phe Gln Glu Tyr Asp Asn His Ile Lys Ser Ser	
70	235 240 245	
71	gtg gtg ggc agt gag cgg aag cga gga atg cag ctg gaa gat ctc aaa	940
72	Val Val Gly Ser Glu Arg Lys Arg Gly Met Gln Leu Glu Asp Leu Lys	
73	250 255 260	
74	cag cag ctc cag cag gcc gag gag gcc ctg gtg gcc aaa cag gag gtg	988
75	Gln Gln Leu Gln Gln Ala Glu Glu Ala Leu Val Ala Lys Gln Glu Val	
76	265 270 275 280	
77	atc gat aag ctg aag gag gag gcc gag cag cac aag att gtg atg gag	1036
78	Ile Asp Lys Leu Lys Glu Glu Ala Glu Gln His Lys Ile Val Met Glu	
79	285 290 295	
80	acc gtt ccg gtg ctg aag gcc cag gcg gat atc tac aag gcg gac ttc	1084
81	Thr Val Pro Val Leu Lys Ala Gln Ala Asp Ile Tyr Lys Ala Asp Phe	
82	300 305 310	
83	cag gct gag agg cag gcc cgg gag aag ctg gcc gag aag gag ctc	1132
84	Gln Ala Glu Arg Gln Ala Arg Glu Lys Leu Ala Glu Lys Lys Glu Leu	
85	315 320 325	
86	ctg cag gag cag ctg gag cag ctg cag agg gag tac agc aaa ctg aag	1180
87	Leu Gln Glu Gln Leu Glu Gln Leu Gln Arg Glu Tyr Ser Lys Leu Lys	
88	330 335 340	
89	gcc agc tgt cag gag tcg gcc agg atc gag gac atg agg aag cgg cat	1228
90	Ala Ser Cys Gln Glu Ser Ala Arg Ile Glu Asp Met Arg Lys Arg His	
91	345 350 355 360	
92	gtc gag gtc tcc cag gcc ccc ttg ccc ccc gcc cct gcc tac ctc tcc	1276
93	Val Glu Val Ser Gln Ala Pro Leu Pro Pro Ala Pro Ala Tyr Leu Ser	
94	365 370 375	

PAGE: 3

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/377,795

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TIME: 12:53:39

Input Set: I377795.RAW

95 tct ccc ctg gcc ctg ccc agc cag agg agg agc ccc ccc gag gag cca 1324  
96 Ser Pro Leu Ala Leu Pro Ser Gln Arg Arg Ser Pro Pro Glu Glu Pro  
97 380 385 390  
98 cct gac ttc tgc tgt ccc aag tgc cag tat cag gcc cct gat atg gac 1372  
99 Pro Asp Phe Cys Cys Pro Lys Cys Gln Tyr Gln Ala Pro Asp Met Asp  
100 395 400 405  
101 acc ctg cag ata cat gtc atg gag tgc att gag tag ggccggccag 1418  
102 Thr Leu Gln Ile His Val Met Glu Cys Ile Glu  
W--> 103 410 415 420  
104 tgcaaggcca ctgcctgccc gaggacgtgc ccgggaccgt gcagtctgcy ctttcctctc 1478  
105 ccgcctgcct agcccaggat gaagggtggt gtggccacaa ctgggatgcc acctggagcc 1538  
106 ccaccagga gctggccgcg gcaccttacg cttcagctgt tgatccgctg gtcccctctt 1598  
107 ttggggtaga tgcggccccg atcaggcctg actcgtctgt ctttttgttc ctttctgtct 1658  
108 gtcgaacca cttgcctcgg gctaatacct ccctcttcct ccaccggca ctggggaagt 1718  
109 caagaatggg gcctggggct ctcagggaga actgcttccc ctggcagagc tgggtggcag 1778  
110 ctcttctcc caccggacac cgaccgcgcc gccgctgtgc cctgggagtg ctgccctctt 1838  
111 accatgcaca cgggtgctct ccttttgggc tgcattgtat tccattttgc agccagaccg 1898  
112 atgtgtattt aaccagtcac tattgatgga catttgggtt gtttcccatc tttttgttac 1958  
113 cataaataat ggcataagtaa aaaaaaaaaa aaaaaa 1994  
114 <210> SEQ ID NO 2  
115 <211> LENGTH: 419  
116 <212> TYPE: PRT  
117 <213> ORGANISM: Homo sapiens  
118 <400> SEQUENCE: 2  
119 Met Asn Arg His Leu Trp Lys Ser Gln Leu Cys Glu Met Val Gln Pro  
120 1 5 10 15  
121 Ser Gly Gly Pro Ala Ala Asp Gln Asp Val Leu Gly Glu Glu Ser Pro  
122 20 25 30  
123 Leu Gly Lys Pro Ala Met Leu His Leu Pro Ser Glu Gln Gly Ala Pro  
124 35 40 45  
125 Glu Thr Leu Gln Arg Cys Leu Glu Glu Asn Gln Glu Leu Arg Asp Ala  
126 50 55 60  
127 Ile Arg Gln Ser Asn Gln Ile Leu Arg Glu Arg Cys Glu Glu Leu Leu  
128 65 70 75 80  
129 His Phe Gln Ala Ser Gln Arg Glu Glu Lys Glu Phe Leu Met Cys Lys  
130 85 90 95  
131 Phe Gln Glu Ala Arg Lys Leu Val Glu Arg Leu Gly Leu Glu Lys Leu  
132 100 105 110  
133 Asp Leu Lys Arg Gln Lys Glu Gln Ala Leu Arg Glu Val Glu His Leu  
134 115 120 125  
135 Lys Arg Cys Gln Gln Gln Met Ala Glu Asp Lys Ala Ser Val Lys Ala  
136 130 135 140  
137 Gln Val Thr Ser Leu Leu Gly Glu Leu Gln Glu Ser Gln Ser Arg Leu  
138 145 150 155 160  
139 Glu Ala Ala Thr Lys Glu Cys Gln Ala Leu Glu Gly Arg Ala Arg Ala  
140 165 170 175  
141 Ala Ser Glu Gln Ala Arg Gln Leu Glu Ser Glu Arg Glu Ala Leu Gln  
142 180 185 190  
143 Gln Gln His Ser Val Gln Val Asp Gln Leu Arg Met Gln Gly Gln Ser  
144 195 200 205

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PAGE: 4

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/377,795

DATE: 04/05/2000  
TIME: 12:53:39

Input Set: I377795.RAW

```

145      Val Glu Ala Ala Leu Arg Met Glu Arg Gln Ala Ala Ser Glu Glu Lys
146          210                      215                      220
147      Arg Lys Leu Ala Gln Leu Gln Val Ala Tyr His Gln Leu Phe Gln Glu
148          225                      230                      235                      240
149      Tyr Asp Asn His Ile Lys Ser Ser Val Val Gly Ser Glu Arg Lys Arg
150          245                      250                      255
151      Gly Met Gln Leu Glu Asp Leu Lys Gln Gln Leu Gln Gln Ala Glu Glu
152          260                      265                      270
153      Ala Leu Val Ala Lys Gln Glu Val Ile Asp Lys Leu Lys Glu Glu Ala
154          275                      280                      285
155      Glu Gln His Lys Ile Val Met Glu Thr Val Pro Val Leu Lys Ala Gln
156          290                      295                      300
157      Ala Asp Ile Tyr Lys Ala Asp Phe Gln Ala Glu Arg Gln Ala Arg Glu
158          305                      310                      315                      320
159      Lys Leu Ala Glu Lys Lys Glu Leu Leu Gln Glu Gln Leu Glu Gln Leu
160          325                      330                      335
161      Gln Arg Glu Tyr Ser Lys Leu Lys Ala Ser Cys Gln Glu Ser Ala Arg
162          340                      345                      350
163      Ile Glu Asp Met Arg Lys Arg His Val Glu Val Ser Gln Ala Pro Leu
164          355                      360                      365
165      Pro Pro Ala Pro Ala Tyr Leu Ser Ser Pro Leu Ala Leu Pro Ser Gln
166          370                      375                      380
167      Arg Arg Ser Pro Pro Glu Glu Pro Pro Asp Phe Cys Cys Pro Lys Cys
168          385                      390                      395                      400
169      Gln Tyr Gln Ala Pro Asp Met Asp Thr Leu Gln Ile His Val Met Glu
170          405                      410                      415
171      Cys Ile Glu
172 <210> SEQ ID NO 3
173 <211> LENGTH: 10
174 <212> TYPE: PRT
175 <213> ORGANISM: Homo sapiens
176 <400> SEQUENCE: 3
177      Ile Val Met Glu Thr Val Pro Val Leu Lys
178          1                      5                      10
179 <210> SEQ ID NO 4
180 <211> LENGTH: 17
181 <212> TYPE: PRT
182 <213> ORGANISM: Homo sapiens
183 <400> SEQUENCE: 4
184      Lys Glu Leu Leu Gln Glu Gln Leu Glu Gln Leu Gln Arg Glu Tyr Ser
185          1                      5                      10                      15
186      Lys
187 <210> SEQ ID NO 5
188 <211> LENGTH: 16
189 <212> TYPE: PRT
190 <213> ORGANISM: Homo sapiens
191 <400> SEQUENCE: 5
192      Glu Leu Leu Gln Glu Gln Leu Glu Gln Leu Gln Arg Glu Tyr Ser Lys
193          1                      5                      10                      15
194 <210> SEQ ID NO 6

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PAGE: 5

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/377,795DATE: 04/05/2000  
TIME: 12:53:39

Input Set: I377795.RAW

195 <211> LENGTH: 20  
196 <212> TYPE: PRT  
197 <213> ORGANISM: Homo sapiens  
198 <400> SEQUENCE: 6  
199 Arg His Val Glu Val Ser Gln Ala Pro Leu Pro Pro Ala Pro Ala Tyr  
200 1 5 10 15  
201 Leu Ser Ser Pro  
202 20  
203 <210> SEQ ID NO 7  
204 <211> LENGTH: 20  
205 <212> TYPE: PRT  
206 <213> ORGANISM: Homo sapiens  
207 <400> SEQUENCE: 7  
208 Leu Ala Gln Leu Gln Val Ala Tyr His Gln Leu Phe Gln Glu Tyr Asp  
209 1 5 10 15  
210 Asn His Ile Lys  
211 20  
212 <210> SEQ ID NO 8  
213 <211> LENGTH: 11  
214 <212> TYPE: PRT  
215 <213> ORGANISM: Homo sapiens  
216 <220> FEATURE:  
217 <221> NAME/KEY: UNSURE  
218 <222> LOCATION: (1)  
219 <400> SEQUENCE: 8  
W--X 220 Xaa Gln Tyr Gln Ala Pro Asp Met Asp Thr Leu  
221 1 5 10  
222 <210> SEQ ID NO 9  
223 <211> LENGTH: 17  
224 <212> TYPE: PRT  
225 <213> ORGANISM: Homo sapiens  
226 <220> FEATURE:  
227 <221> NAME/KEY: UNSURE  
228 <222> LOCATION: (1)  
229 <400> SEQUENCE: 9  
W--X 230 Xaa Gln Pro Ser Gly Gly Pro Ala Ala Asp Gln Asp Val Leu Gly Glu  
231 1 5 10 15  
232 Glu  
233 <210> SEQ ID NO 10  
234 <211> LENGTH: 13  
235 <212> TYPE: PRT  
236 <213> ORGANISM: Homo sapiens  
237 <400> SEQUENCE: 10  
238 Gln Gln Leu Gln Gln Ala Glu Glu Ala Leu Val Ala Lys  
239 1 5 10  
240 <210> SEQ ID NO 11  
241 <211> LENGTH: 11  
242 <212> TYPE: PRT  
243 <213> ORGANISM: Homo sapiens  
244 <400> SEQUENCE: 11

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I377795.RAW

Line	? Error/Warning	Original Text
103	W Invalid/Missing Amino Acid Numbering	410 415
220	W "N" or "Xaa" used: Feature required	Xaa Gln Tyr Gln Ala Pro Asp Met Asp Thr L
230	W "N" or "Xaa" used: Feature required	Xaa Gln Pro Ser Gly Gly Pro Ala Ala Asp G
269	W "N" or "Xaa" used: Feature required	Xaa Xaa Val Thr Ser Leu Leu Gly Glu Leu G
279	W "N" or "Xaa" used: Feature required	Xaa Xaa Leu Gln Gln Ala Glu Glu Ala Leu V
298	W "N" or "Xaa" used: Feature required	Xaa Gln Val Thr Xaa Leu Leu Xaa Glu Leu G
308	W "N" or "Xaa" used: Feature required	Xaa Ala Gln Leu Gln Val Ala Tyr His Gln L